

OIIPE

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## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/899,634A

TIME: 16:19:12

Input Set : A:\SEQ IDs of application 4\_31499A.txt

Output Set: N:\CRF3\12062001\I899634A.raw

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3 <110> APPLICANT: Thomas Buehler, Reto Andreas Gadiant, Reinhard Korn, Rao Movva  
W--> 4 <120> TITLE OF INVENTION: pCAR and its uses  
6 <130> FILE REFERENCE: 4-31499A  
C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/899,634A  
C--> 8 <141> CURRENT FILING DATE: 2001-07-05  
8 <160> NUMBER OF SEQ ID NOS: 4  
10 <170> SOFTWARE: PatentIn version 3.0  
12 <210> SEQ ID NO: 1  
13 <211> LENGTH: 4286  
14 <212> TYPE: DNA  
15 <213> ORGANISM: porcine  
17 <220> FEATURE:  
18 <221> NAME/KEY: CDS  
19 <222> LOCATION: (3229)..(4014)  
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26	agttgggac	tttgcatgg	cccacggctc	tcaggatggg	gatgctcccc	ttcagcaccc	180
28	ggttccccct	ggaaactgat	ggctcctggc	ctgtggcatg	gcagtggcac	tgtgaggagc	240
30	ccctaccagc	agcacacagt	gggtttggca	ctgccacgct	ccggatgcgc	cgctctgac	300
32	caaccccata	atcaagggaa	ccgaattgc	cccatcattg	ccccaccac	ccccatcctg	360
34	ccgggccctc	acaccccacg	ctgccttggt	gtgacattcc	ccagcccaaa	cccacggcct	420
36	catggctacc	gcggggcatt	tcccattgcc	gccccattat	cagctctgca	cacctccgc	480
38	tgtacccatg	cctcgtggct	gccttctttt	gacgtataat	cttctaatta	ataccggcc	540
40	ttgtcaaagt	ggagcaca	cgtaattaa	ttccccagca	ggcaggta	taacagtgtg	600
42	actccctttt	tgtcgcag	ggggctgata	cagagagatg	tggcactatg	gagcccacgg	660
44	ggctcctggc	ctgggtgccc	acggagggtc	ccatgtgctg	cagtgtcacc	gcctccgagg	720
46	tgacagtatt	gtccctgcgg	tgccctgca	gtcagctct	gtccacagg	ccacctccag	780
48	tttggagggg	acacaatgca	gccccgatgc	aaccatcct	cgcagcatcc	caggga	840
50	gacccactg	caagaccgca	cacagggtg	ggtccgcctc	ccctaata	tacagtgtt	900
52	ttgcatggcc	ccttaatcaa	tgcagtta	cagcatgcgc	tcatgcaccg	ctctggagct	960
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62	ctgaggtgca	cccagcagtg	cactcagcag	tccaagggcc	ggcctggagg	tttgaccgc	1260
64	tacgtgctga	cattagcatt	gaacttggcc	ctgggtagtg	ctgcaggccg	ggcgggggtg	1320
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68	ggctgcaccc	cagcaccagg	ccggtgcatg	catgctcctg	gtgttattgc	agcctgggtg	1440
70	atgcatgcgt	cttagtggtg	cagcgcgtg	catgcattcc	ccttggtgtg	tagcagctta	1500
72	gtgcatgcat	acccctcggt	gttattgctg	ctctgtgcac	gcacgctcat	tgtatcactt	1560
74	catcccagtg	catgcactca	cactggagcg	attgctgctc	ggtgcacgca	cactcattgt	1620
76	atcacgtcag	ctcagtggct	gcacgcacac	cgggtgtatt	gctgctcggt	gcgtgcatgc	1680
78	acatcagtgt	cgtgcagct	cagtgcagtc	acgctcattg	cccatcgcta	tccctgcctc	1740
80	tccctgctgg	gctccccggg	aggtgacttc	aaggggaccg	caggaccacc	tcgggggtgg	1800
82	ggggagggct	gcacacgcgg	accccgctcc	ccctccccaa	caaagcactg	tggaatcaaa	1860
84	aaggggggag	gggggatgga	ggggcgcgct	acacccccgc	cccacaccct	cacctcgagg	1920

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86 tgagccccac gttctgcttc actctcccca tctccccccc ctccccaccc ccaattttgt 1980
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90 ccaggcgggg cggggcgggg cgaggggcgg ggcggggcga ggcggagagg tgcggcggca 2100
92 gccaatcaga gcggcgcgct ccgaaagttt ccttttatgg cgaggcggcg gcggcggcg 2160
94 ccctataaaa agcgaagcgc gcggcggggc ggagtcgctg cgttgccctc gccccgtgcc 2220
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102 ggggggggagc ggctcggggg gtgcgtgcgt gtgtgtgtgc gtggggagcg ccgcgtgcgg 2460
104 cccgcgctgc ccggcggtcg tgagcgctgc gggcgcgggc cggggctttg tgcgtccgc 2520
106 gtgtgcgcga ggggagcgcg gccggggggc gtgcccgcgc gtgcgggggg gctgcgagg 2580
108 gaacaaaggc tgcgtgcggg gtgtgtgcgt gggggggtga gcagggggtg tgggcgcggc 2640
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120 aaatctggga ggcgcgcgcg cccccctct agcgggcgcg ggcgaagcgg tgcggcgccg 3000
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128 cagcccccaa gcttaagggt cacggcccac gtggggacta gtgccacc atg gcg ctc 3237
129                                     Met Ala Leu
130                                     1
132 ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc acc aga agt 3285
133 Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu Thr Arg Ser
134 5 10 15
136 ttg agt atc act act cct gaa cag atg att gaa aag gcc aaa ggg gaa 3333
137 Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala Lys Gly Glu
138 20 25 30 35
140 act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa gac cag ggg 3381
141 Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu Asp Gln Gly
142 40 45 50
144 ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat cag aag gtg 3429
145 Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn Gln Lys Val
146 55 60 65
148 gat caa gtg att att tta tat tct gga gac aaa att tat gac gac tac 3477
149 Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr Asp Asp Tyr
150 70 75 80
152 tac caa gat ctg aaa gga cga gta cat ttt aca agt aat gat ctc aaa 3525
153 Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn Asp Leu Lys
154 85 90 95
156 tca ggt gat gca tca ata aat gta aca aat cta cag ttg tca gat att 3573
157 Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu Ser Asp Ile
158 100 105 110 115
160 ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt gga aat aag 3621
161 Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val Gly Asn Lys
162 120 125 130
164 aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca aga tgt tat 3669

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165 Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr Arg Cys Tyr
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168 gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta aaa tgt gaa 3717
169 Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu Lys Cys Glu
170      150      155      160
172 cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag aaa ttg tcc 3765
173 Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln Lys Leu Ser
174      165      170      175
176 aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg act tca cct 3813
177 Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met Thr Ser Pro
178 180      185      190      195
180 gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg aca tac agc 3861
181 Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly Thr Tyr Ser
182      200      205      210
184 tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg ctt cgc ctg 3909
185 Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu Leu Arg Leu
186      215      220      225
188 gat gtg gtt cct cct tca aat aga gct gga aca att gca gga gct gtt 3957
189 Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala Gly Ala Val
190      230      235      240
192 ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt atc atc ttt tgc 4005
193 Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile Ile Phe Cys
194      245      250      255
196 tgt cgt taa tctagataag taatgatcat aatcagccat atcacatctg 4054
197 Cys Arg
198 260
200 tagagggtttt acttgcttta aaaaacctcc cacacctccc cctgaacctg aaacataaaa 4114
202 tgaatgcaat tgttggttgtt aacttgcttta ttgcagctta taatgggttac aaataaagca 4174
204 atagcatcac aaatttcaca aataaagcat ttttttcaact gcattctagt tgtggtttgt 4234
206 ccaaactcat caatgtatct tatcatgtct ggatccccgg gtaccgagct cg 4286
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211 <212> TYPE: PRT
212 <213> ORGANISM: porcine
214 <400> SEQUENCE: 2
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221      20      25      30
224 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
225      35      40      45
228 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
229      50      55      60
232 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
233 65      70      75      80
236 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
237      85      90      95
240 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
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248 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
249      130      135      140
252 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
253 145      150      155      160
256 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
257      165      170      175
260 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
261      180      185      190
264 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
265      195      200      205
268 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
269      210      215      220
272 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
273 225      230      235      240
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277      245      250      255
280 Ile Phe Cys Cys Arg
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286 <210> SEQ ID NO: 3
287 <211> LENGTH: 1098
288 <212> TYPE: DNA
289 <213> ORGANISM: porcine

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W--> 290 <220> FEATURE:
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292 <222> LOCATION: (1)..(1098)
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297 1      5      10      15
299 acc aga agt ttg agt atc act act cct gaa cag atg att gaa aag gcc      96
300 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
301      20      25      30
303 aaa ggg gaa act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa      144
304 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
305      35      40      45
307 gac cag ggg ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat      192
308 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
309      50      55      60
311 cag aag gtg gat caa gtg att att tta tat tct gga gac aaa att tat      240
312 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
313 65      70      75      80
315 gac gac tac tac caa gat ctg aaa gga cga gta cat ttt aca agt aat      288
316 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
317      85      90      95
319 gat ctc aaa tca ggt gat gca tca ata aat gta aca aat cta cag ttg      336
320 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
321      100      105      110

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327 gga aat aag aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca      432
328 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
329      130      135      140
331 aga tgt tat gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta      480
332 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
333      145      150      155      160
335 aaa tgt gaa cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag      528
336 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
337      165      170      175
339 aaa ttg tcc aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg      576
340 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
341      180      185      190
343 act tca cct gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg      624
344 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
345      195      200      205
347 aca tac agc tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg      672
348 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
349      210      215      220
351 ctt cgc ctg gat gtg gtt cct cct tca aat aga gct gga aca att gca      720
352 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
353      225      230      235      240
355 gga gct gtt ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt att      768
356 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
357      245      250      255
359 gtg ttt tgc tgt cat aaa aag cgc aga gaa gaa aaa tac gaa aaa gaa      816
360 Val Phe Cys Cys His Lys Lys Arg Arg Glu Glu Lys Tyr Glu Lys Glu
361      260      265      270
363 gtg cat cat gat atc agg gaa gac gtg cct cct ccg aag agc aga acg      864
364 Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr
365      275      280      285
367 tcc act gcc aga agc tac ctc ggc agc aac cac tcg tcc ctg gga tcc      912
368 Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser
369      290      295      300
371 atg tct cct tcc aac atg gaa ggc tat tcc aag act cag tat aac cag      960
372 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln
373      305      310      315      320
375 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg      1008
376 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro
377      325      330      335
379 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct      1056
380 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro
381      340      345      350
383 gtg atg att cca gcc cag agc aag gac ggg tcc ata gta taa      1098
384 Val Met Ile Pro Ala Gln Ser Lys Asp Gly Ser Ile Val
385      355      360      365
389 <210> SEQ ID NO: 4

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L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
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